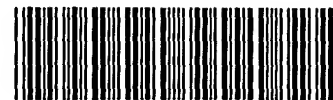


0570
0617

#10



OIPE

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/057,467

TIME: 14:04:49

Input Set : N:\Crf3\RULE60\10057467.raw

Output Set: N:\CRF3\07022002\J057467.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Nolan, Garry P.

6 Rothenberg, Michael S.

8 (ii) TITLE OF INVENTION: Methods for Screening for Transdominant

9 Effector Peptides and RNA Molecules

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

15 (B) STREET: 4 Embarcadero Center, Suite 3400

16 (C) CITY: San Francisco

17 (D) STATE: CA

18 (E) COUNTRY: USA

19 (F) ZIP: 94111-4187

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

ENTERED

C--> 28 (A) APPLICATION NUMBER: US/10/057,467

C--> 29 (B) FILING DATE: 22-Jan-2002

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/589,109

34 (B) FILING DATE: 23-JAN-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Silva, Robin M.

40 (B) REGISTRATION NUMBER: 38,304

41 (C) REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (415) 781-1989

45 (B) TELEFAX: (415) 949-8711

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 9 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS:

W--> 53 (D) TOPOLOGY: Not Relevant

55 (ii) MOLECULE TYPE: peptide

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 59 Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa

60 1

5

RAW SEQUENCE LISTING

DATE: 07/02/2002

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Input Set : N:\Crf3\RULE60\10057467.raw

Output Set: N:\CRF3\07022002\J057467.raw

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62 (2) INFORMATION FOR SEQ ID NO: 2:
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66       (B) TYPE: nucleic acid
67       (C) STRANDEDNESS: double
68       (D) TOPOLOGY: linear
70   (ii) MOLECULE TYPE: cDNA
72   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74 GCTTAGCAAG ATCTCTACGG TGGACCKNNK NNNNNNNNNK NNNNNNNNNK KNNNNNCCCC 60
76 ACTCCCATGG TCCTACGTAC CACCACACTG GG 92
78 (2) INFORMATION FOR SEQ ID NO: 3:
80   (i) SEQUENCE CHARACTERISTICS:
81       (A) LENGTH: 34 base pairs
82       (B) TYPE: nucleic acid
83       (C) STRANDEDNESS: double
84       (D) TOPOLOGY: linear
86   (ii) MOLECULE TYPE: cDNA
88   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
90 GCTTAGCAAG ATCTGTGTGT CAGTTAGGGT GTGG 34
92 (2) INFORMATION FOR SEQ ID NO: 4:
94   (i) SEQUENCE CHARACTERISTICS:
95       (A) LENGTH: 74 base pairs
96       (B) TYPE: nucleic acid
97       (C) STRANDEDNESS: double
98       (D) TOPOLOGY: linear
100  (ii) MOLECULE TYPE: cDNA
102  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
104 CTGGAGAACC AGGACCATGG GCNNKNNKNN KNNKNNKNNK NNNNNNNNNK NKGGGCCCCC 60
106 TTAAACCATT AAAT 74
108 (2) INFORMATION FOR SEQ ID NO: 5:
110   (i) SEQUENCE CHARACTERISTICS:
111       (A) LENGTH: 71 base pairs
112       (B) TYPE: nucleic acid
113       (C) STRANDEDNESS: double
114       (D) TOPOLOGY: linear
116   (ii) MOLECULE TYPE: cDNA
118   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
120 CTGGAGAACC AGGACCATGG GCNNKNNKNN KCCTCCCNK CCTNNKNNKG GGCCCCCTTA 60
122 AACCATTAAA T 71
124 (2) INFORMATION FOR SEQ ID NO: 6:
126   (i) SEQUENCE CHARACTERISTICS:
127       (A) LENGTH: 26 base pairs
128       (B) TYPE: nucleic acid
129       (C) STRANDEDNESS: double
130       (D) TOPOLOGY: linear
132   (ii) MOLECULE TYPE: cDNA
134   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
136 TCATGCATCC AATTTAATGG TTAAAG 26
138 (2) INFORMATION FOR SEQ ID NO: 7:

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RAW SEQUENCE LISTING

DATE: 07/02/2002

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Input Set : N:\Crf3\RULE60\10057467.raw

Output Set: N:\CRF3\07022002\J057467.raw

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140      (i) SEQUENCE CHARACTERISTICS:
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142          (B) TYPE: nucleic acid
143          (C) STRANDEDNESS: double
144          (D) TOPOLOGY: linear
146      (ii) MOLECULE TYPE: DNA (genomic)
148      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
150  TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCAT      60
152  GGAAAATACA TAACTGAGAA TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCA      120
154  GAATATGGGC CAAACAGGAT ATCTGTGGTA AGCAGTTCCT GCCCCGGCTC AGGGCCAAGA      180
156  ACAGATGGTC CCCAGATGCG GTCCCGCCCT CAGCAGTTTC TAGAGAACCA TCAGATGTTT      240
158  CCAGGGTGCC CCAAGGACCT GAAATGACC CTGTGCCCTTA TTTGAACTAA CCAATCAGTT      300
160  CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC TCCCCGAGCT CAATAAAAGA GCCCACAACC      360
162  CCTCACTCGG CGCGCCAGTC CTCGATAGA CTGCGTCGCC CGGGTACCCG TATTCCTCAAT      420
164  AAAGCCTCTT GCTGTTTGCA TCCGAATCGT GGACTCGCTG ATCCTTGGGA GGGTCTCCTC      480
166  AGATTGATTG ACTGCCCACC TCGGGGGTCT TTCATTGGA GGTTCACCG AGATTTGGAG      540
168  ACCCTGCCT AGGGACCACC GACCCCCCG CCGGGAGGTA AGCTGGCCAG CGGTCTGTTT      600
170  CTGTCTGTCT CTGTCTTTGT GCGTGTGTTG GCCGGCATCT AATGTTTGCG CCTGCGTCTG      660
172  TACTAGTTAG CTAAGTAGCT CTGTATCTGG CGGACCCGTG GTGGAAGTGA CGAGTTCTGA      720
174  ACACCCGGCC GCAACCTGG GAGACGTCCC AGGGACTTTG GGGGCCGTTT TTGTGGCCCG      780
176  ACCTGAGGAA GGGAGTCGAT GTGGAATCCG ACCCCGTCAG GATATGTGGT TCTGGTAGGA      840
178  GACGAGAACC TAAACAGTT CCCGCTCCG TCTGAATTTT TGCTTTCGGT TTGGAACCGA      900
180  AGCCGCGCGT CTGTCTGCT GCAGCGCTGC AGCATCGTTC TGTGTTCTCT CTGTCTGACT      960
182  GTGTTTCTGT ATTTGTCTGA AAATTAGGGC CAGACTGTGA CCATCCCTT AAGTTTGACC      1020
184  TTAGGTCACT GGAAAGATGT CGAGCGGATC GCTCACAAAC AGTCGGTAGA TGTCAAGAAG      1080
186  AGACGTTGGG TTACCTTCTG CTCTGCAGAA TGGCCAACTT TTAACGTCGG ATGGCCGCGA      1140
188  GACGGCACCT TTAACCGAGA CCTCATCACC CAGGTTAAGA TCAAGGTCTT TTCACCTGGC      1200
190  CCGCATGGAC ACCCAGACCA GGTCCCCTAC ATCGTGACCT GGAAGCCTT GGCTTTTGAC      1260
192  CCCCCTCCCT GGGTCAAGCC CTTGTACAC CCTAAGCCTC CGCTCTCTCT TCCTCCATCC      1320
194  GCCCCGTCTC TCCCCCTTGA ACCTCCTCGT TCGACCCCGC CTCGATCCTC CCTTTATCCA      1380
196  GCCCTCACTC TTTCTCTAGG CGCCGGAATT CCAGGACCAT GGGCGGGCCC CCTTAAACCA      1440
198  TTAAATTGGT AAAATAAAGG ATCCGTCGAC CTGCAGCCAA GCTTATCGAT AAAATAAAG      1500
200  ATTTTATTTA GTCTCCAGAA AAAGGGGGGA ATGAAAGACC CCACCTGTAG GTTTGGCAAG      1560
202  CTAGCTTAAG TAACGCCATT TTGCAAGGCA TGGAAAATAC ATAAGTGA ATAGAGAAGT      1620
204  TCAGATCAAG GTTAGGAACA GAGAGACAGC AGAATATGGG CCAAACAGGA TATCTGTGGT      1680
206  AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG AACAGATGGT CCCCAGATGC GGTCCCGCCC      1740
208  TCAGCAGTTT CTAGAGAACC ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAGTAC      1800
210  CCTGTGCTT ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCTG CGCGCTTCTG      1860
212  CTCCCCGAGC TCAATAAAG AGCCACAAC CCCTCACTCG GCGCGCCAGT CCTCCGATAG      1920
214  ACTGCGTCGC CCGGGTACCC GTGTATCCAA TAAACCTCT TGCAGTTGCA TCCGACTTGT      1980
216  GGTCTCGCTG TTCCTTGGGA GGTCTCCTC TGAGTGATTG ACTACCCGTC AGCGGGGGTC      2040
218  TTTCATTCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAATT      2100
220  CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT GGGGTGCCTA ATGAGTGAGC      2160
222  TAAGTACAT TAATTCGCTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA CCTGTCGTGC      2220
224  CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT      2280
226  TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGTCTGTTT GGCTGCGGCG AGCGGTATCA      2340
228  GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC      2400
230  ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT      2460
232  TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAATC GACGCTCAAG TCAGAGGTGG      2520

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RAW SEQUENCE LISTING

DATE: 07/02/2002

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234 CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC 2580
236 TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTCTCTCC TTCGGGAAGC 2640
238 GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC 2700
240 AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCCGACC GCTGCGCCTT ATCCGGTAAC 2760
242 TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT 2820
244 AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT 2880
246 AACTACGGCT AACTAGAAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC 2940
248 TTCGGAAGAA GAGTTGGTAG CTCTTGATCC GGCAACAAA CCACCGCTGG TAGCGGTGGT 3000
250 TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAG GATCTCAAGA AGATCCTTTG 3060
252 ATCTTTTCTA CCGGGTCTGA CGCTCAGTGG AACGAAACT CACGTTAAGG GATTTTGGTC 3120
254 ATGAGATTAT CAAAAAGGAT CTTCACTAG ATCCTTTTAA ATTAAAAATG AAGTTTAAA 3180
256 TCAATCTAAA GTATATATGA GTAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG 3240
258 GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG TTGCCTGACT CCCCCTCGTG 3300
260 TAGATAACTA CGATACGGGA GGGCTTACCA GTGCGCCCA GTGCTGCAAT GATACCGCGA 3360
262 GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAAC AGCCAGCCGG AAGGGCCGAG 3420
264 CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA 3480
266 GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC 3540
268 ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA 3600
270 AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG 3660
272 ATCGTTGTCA GAAGTAAGTT GGCCGAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT 3720
274 AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGA CTGTTGTA GTACTCAACC 3780
276 AAGTCATTCT GAGAATAGTG TATGCGCGCA CCGAGTTGCT CTGCCCCGGC GTCAATACGG 3840
278 GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG 3900
280 GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT 3960
282 GCACCCAAC TATCTTCAGC ATCTTTTACT TTCACCGCG TTTCTGGGTG AGCAAAAACA 4020
284 GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA 4080
286 CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGT ATTGTCTCAT GAGCGGATAC 4140
288 ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTT CGCGCACATT TCCCCGAAAA 4200
290 GTGCCACCTG ACGTCTAAGA AACCATATT ATCATGACAT TAACCTATAA AAATAGGCGT 4260
292 ATCACGAGGC CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG 4320
294 CAGCTCCCGG AGACGGTCAC AGCTTGCTCT TAAGCGGATG CCGGGAGCAG ACAAGCCCGT 4380
296 CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCTGGC TTAACATATG GGCATCAGAG 4440
298 CAGATTGTAC TGAGAGTGCA CCATATGCGG TGTGAAATAC CGCACAGATG CGTAAGGAGA 4500
300 AAATACCGCA TCAGGCGCCA TTCGCCATTG AGGCTGCGCA ACTGTTGGGA AGGGCGATCG 4560
302 GTGCGGGCCT CTTCTGCTATT ACGCCAGCTG GCGAAAGGGG GATGTGCTGC AAGGCGATTA 4620
304 AGTTGGGTAA CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGCCACG 4680
306 CTCTCCCTTA TGCGACTCCT GCATTAGGAA GCAGCCAGT AGTAGGTTGA GGCCGTTGAG 4740
308 CACCGCCGCC GCAAGGAATG GTGCATGCAA GGAGATGGCG CCCAACAGTC CCCCAGCCAC 4800
310 GGGGCTGCC ACCATACCCA CGCGAAACA AGCGCTCATG AGCCGAAGT GGCGAGCCCG 4860
312 ATCTTCCCCA TCGGTGATGT CGGCGATATA GGCGCCAGCA ACCGCACCTG TGGCGCCGGT 4920
314 GATGCCGGCC ACGATGCGTC CGGCGTAGAG 4950

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316 (2) INFORMATION FOR SEQ ID NO: 8:

318 (i) SEQUENCE CHARACTERISTICS:

319 (A) LENGTH: 7 amino acids

320 (B) TYPE: amino acid

321 (C) STRANDEDNESS:

W--> 322 (D) TOPOLOGY: Not Relevant

324 (ii) MOLECULE TYPE: peptide

326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/057,467

TIME: 14:04:49

Input Set : N:\Crf3\RULE60\10057467.raw

Output Set: N:\CRF3\07022002\J057467.raw

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328   Pro Lys Lys Lys Arg Lys Val
329     1           5
331 (2) INFORMATION FOR SEQ ID NO: 9:
332   (i) SEQUENCE CHARACTERISTICS:
333     (A) LENGTH: 20 amino acids
334     (B) TYPE: amino acid
335     (C) STRANDEDNESS:
336     (D) TOPOLOGY: Not Relevant
W--> 337
338   (ii) MOLECULE TYPE: peptide
339   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
340   Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
341     1           5           10           15
342   Lys Lys Leu Asp
343     20
344 (2) INFORMATION FOR SEQ ID NO: 10:
345   (i) SEQUENCE CHARACTERISTICS:
346     (A) LENGTH: 4 amino acids
347     (B) TYPE: amino acid
348     (C) STRANDEDNESS:
349     (D) TOPOLOGY: Not Relevant
W--> 350
351   (ii) MOLECULE TYPE: peptide
352   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
353   Gly Gly Pro Pro
354     1
355 (2) INFORMATION FOR SEQ ID NO: 11:
356   (i) SEQUENCE CHARACTERISTICS:
357     (A) LENGTH: 48 base pairs
358     (B) TYPE: nucleic acid
359     (C) STRANDEDNESS: unknown
360     (D) TOPOLOGY: unknown
361   (ii) MOLECULE TYPE: cDNA
362   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
363   ATGGGAAAGA AGAAGAAGAA GAAGAAGAAG AAGAAGGGGG GGCCCCCC
364     48
365 (2) INFORMATION FOR SEQ ID NO: 12:
366   (i) SEQUENCE CHARACTERISTICS:
367     (A) LENGTH: 30 base pairs
368     (B) TYPE: nucleic acid
369     (C) STRANDEDNESS: unknown
370     (D) TOPOLOGY: unknown
371   (ii) MOLECULE TYPE: cDNA
372   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
373   CCTCCTCCTC CTCCTCCTCC TCCTCCTCCT
374     30
375 (2) INFORMATION FOR SEQ ID NO: 13:
376   (i) SEQUENCE CHARACTERISTICS:
377     (A) LENGTH: 30 base pairs
378     (B) TYPE: nucleic acid
379     (C) STRANDEDNESS: unknown
380     (D) TOPOLOGY: unknown
381   (ii) MOLECULE TYPE: cDNA
382   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
383   CCTCCTCCTC CTCCTCCTCC TCCTCCTCCT
384     30
385 (2) INFORMATION FOR SEQ ID NO: 14:
386   (i) SEQUENCE CHARACTERISTICS:
387     (A) LENGTH: 30 base pairs
388     (B) TYPE: nucleic acid
389     (C) STRANDEDNESS: unknown
390     (D) TOPOLOGY: unknown
391   (ii) MOLECULE TYPE: cDNA
392   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
393   CCTCCTCCTC CTCCTCCTCC TCCTCCTCCT
394     30
395 (2) INFORMATION FOR SEQ ID NO: 15:
396   (i) SEQUENCE CHARACTERISTICS:
397     (A) LENGTH: 30 base pairs
398     (B) TYPE: nucleic acid
399     (C) STRANDEDNESS: unknown
400     (D) TOPOLOGY: unknown
401   (ii) MOLECULE TYPE: cDNA
402   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
403   CCTCCTCCTC CTCCTCCTCC TCCTCCTCCT
404     30

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/02/2002
PATENT APPLICATION: US/10/057,467 TIME: 14:04:50

Input Set : N:\Crf3\RULE60\10057467.raw
Output Set: N:\CRF3\07022002\J057467.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.1,2,3,6,8,9

Seq#:2; N Pos. 28,29,31,32,34,35,37,38,40,41,43,44,46,47,49,50,52,53,55,56

Seq#:4; N Pos. 23,24,26,27,29,30,32,33,35,36,38,39,41,42,44,45,47,48,50,51

Seq#:5; N Pos. 23,24,26,27,29,30,38,39,44,45,47,48

Seq#:13; N Pos. 3,6,9,12,15,18,21,24,27,30

Seq#:14; N Pos. 3,6,9,12,15,18,21,24,27,30

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/057,467

DATE: 07/02/2002

TIME: 14:04:50

Input Set : N:\Crf3\RULE60\10057467.raw

Output Set: N:\CRF3\07022002\J057467.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:53 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:322 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:337 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:355 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10